

(2)

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,766

DATE: 07/24/2001.
TIME: 10:47:32

Input Set : A:\Seq.txt
Output Set: N:\CRF3\07242001\I900766.raw

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3 <110> APPLICANT: FORSBERG, GORAN
4      ERLANDSSON, EVA
5      ANTONSSON, PER
6      WALSE, BJORN
8 <120> TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
10 <130> FILE REFERENCE: P02188US0;10104199
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/900,766
C--> 13 <141> CURRENT FILING DATE: 2001-07-06
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 672
21 <212> TYPE: PRT
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <221> NAME/KEY: PEPTIDE
26 <222> LOCATION: (1)..(672)
27 <223> OTHER INFORMATION: Conjugate protein
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32 Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala
33 1          5          10          15
35 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
36          20          25          30
38 Tyr Met His Trp Val Lys Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
39          35          40          45
41 Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe
42          50          55          60
44 Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
45 65          70          75          80
47 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
48          85          90          95
50 Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln
51          100         105         110
53 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
54          115         120         125
56 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
57          130         135         140
59 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
60 145          150          155          160
62 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
63          165          170          175
65 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
66          180          185          190
68 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
69          195          200          205
71 Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Ser Gly Gly
72          210          215          220

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74 Pro Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys
75 225 230 235 240
77 Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr
78 245 250 255
80 Tyr Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe
81 260 265 270
83 Leu Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp
84 275 280 285
86 Tyr Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu
87 290 295 300
89 Tyr Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln
90 305 310 315 320
92 Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val
93 325 330 335
95 Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile
96 340 345 350
98 Asn Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val
99 355 360 365
101 Lys Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala
102 370 375 380
104 Arg His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe
105 385 390 395 400
107 Gly Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly
108 405 410 415
110 Ser Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp
111 420 425 430
113 Thr Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser
114 435 440 445
116 Leu Ser Ile Ser Leu Tyr Leu Tyr Thr Thr Ser Ile Val Met Thr Gln
117 450 455 460
119 Thr Pro Thr Ser Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr
120 465 470 475 480
122 Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln
123 485 490 495
125 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Thr Ser Ser Arg
126 500 505 510
128 Tyr Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp
129 515 520 525
131 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Val Tyr
132 530 535 540
134 Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Thr
135 545 550 555 560
137 Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe
138 565 570 575
140 Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
141 580 585 590
143 Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
144 595 600 605
146 Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln

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147      610          615          620
149 Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
150 625           630           635           640
152 Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
153           645           650           655
155 Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Ser
156           660           665           670
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 233
160 <212> TYPE: PRT
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164 <221> NAME/KEY: Peptide
165 <222> LOCATION: (1)..(233)
166 <223> OTHER INFORMATION: Chimeric Protein
169 <400> SEQUENCE: 2
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172 1           5           10           15
174 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
175 20          25          30
177 Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe Leu
178 35          40          45
180 Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
181 50          55          60
183 Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu Tyr
184 65          70          75          80
186 Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
187 85          90          95
189 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
190 100         105         110
192 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
193 115         120         125
195 Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
196 130         135         140
198 Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
199 145         150         155         160
201 His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
202 165         170         175
204 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
205 180         185         190
207 Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
208 195         200         205
210 Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser Leu
211 210         215         220
213 Ser Ile Ser Leu Tyr Leu Tyr Thr Thr
214 225         230
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 233
218 <212> TYPE: PRT

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Input Set : A:\Seq.txt
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219 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: peptide
222 <222> LOCATION: (1)..(233)
223 <223> OTHER INFORMATION: Chimeric Protein
227 <400> SEQUENCE: 3
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230 1 5 10 15
232 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
233 20 25 30
235 Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
236 35 40 45
238 Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
239 50 55 60
241 Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
242 65 70 75 80
244 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
245 85 90 95
247 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Val Thr
248 100 105 110
250 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
251 115 120 125
253 Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
254 130 135 140
256 Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
257 145 150 155 160
259 His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
260 165 170 175
262 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
263 180 185 190
265 Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
266 195 200 205
268 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu
269 210 215 220
271 His Ile Ala Leu Tyr Leu Tyr Thr Thr
272 225 230
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 233
276 <212> TYPE: PRT
277 <213> ORGANISM: Staphylococcus sp.
279 <400> SEQUENCE: 4
281 Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
282 1 5 10 15
284 Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr
285 20 25 30
287 Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu
288 35 40 45
290 Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp His Ser Trp Tyr
291 50 55 60

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293 Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr
294 65 70 75 80
296 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
297 85 90 95
299 Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
300 100 105 110
302 Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
303 115 120 125
305 Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys
306 130 135 140
308 Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
309 145 150 155 160
311 Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
312 165 170 175
314 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro
315 180 185 190
317 Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser Asn Thr
318 195 200 205
320 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met
321 210 215 220
323 His Ile Asp Ile Tyr Leu Tyr Thr Ser
324 225 230
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 203
328 <212> TYPE: PRT
329 <213> ORGANISM: Staphylococcus sp.
331 <400> SEQUENCE: 5
333 Ala Leu His Lys Lys Ser Glu Leu Ser Ser Thr Ala Leu Asn Asn Met
334 1 5 10 15
336 Lys His Ser Tyr Ala Asp Ala Asn Pro Ile Ile Gly Ala Asn Lys Ser
337 20 25 30
339 Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu Leu Tyr Lys Ala Phe Phe
340 35 40 45
342 Leu Leu Ile Asn Phe Asn Ser Ala Glu Met Ala Gln His Phe Lys Ser
343 50 55 60
345 Lys Asn Val Asp Val Tyr Ala Ile Arg Tyr Ala Ala Ala Cys Arg Thr
346 65 70 75 80
348 Ala Cys Thr Tyr Gly Gly Val Thr Pro His Ala Gly Asn Ala Leu Lys
349 85 90 95
351 Ala Arg Lys Lys Ile Pro Ile Asn Leu Trp Ile Ile Gly Val Gln Lys
352 100 105 110
354 Glu Val Ser Leu Asp Lys Val Gln Thr Asp Lys Lys Asn Val Thr Val
355 115 120 125
357 Gln Glu Leu Asp Ala Gln Ala Arg Arg Tyr Leu Gln Lys Asp Leu Lys
358 130 135 140
360 Leu Tyr Asn Ala Ile Gln Arg Gly Lys Leu Glu Phe Asp Ser Ala Ala
361 145 150 155 160
363 Ala Ser Lys Val Ser Tyr Asp Leu Phe Asp Val Ala Gly Asp Phe Pro
364 165 170 175

VERIFICATION SUMMARY
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Input Set : A:\Seq.txt
Output Set: N:\CRF3\07242001\I900766.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date